```
### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.01.00D

Last logoff:  19mar04 16:47:45
Logon file001 23mar04 14:36:05
           *** ANNOUNCEMENT ***
                     ***
--File 654 - US published applications from March 15, 2001 to the
present are now online.  Please see HELP NEWS 654 for details.

                     ***
--File 581 - The 2003 annual reload of Population Demographics is
complete. Please see Help News581 for details.

                    ***
--File 990 - NewsRoom now contains February 2003 to current records.
File 992 - NewsRoom 2003 archive has been newly created and contains
records from January 2003. The oldest months's records roll out of
File 990 and into File 992 on the first weekend of each month.
To search all 2003 records BEGIN 990, 992, or B NEWS2003, a new
OneSearch category.
                     ***
--Connect Time joins DialUnits as pricing options on Dialog.
See HELP CONNECT for information.
                     ***
                     ***
--SourceOne patents are now delivered to your email inbox
as PDF replacing TIFF delivery. See HELP SOURCE1 for more
information.
                     ***
--Important news for public and academic
libraries.  See HELP LIBRARY for more information.
                     ***
--Important Notice to Freelance Authors--
See HELP FREELANCE for more information
                     ***
NEW FILES RELEASED
***DIOGENES: Adverse Drug Events Database (File 181)
***World News Connection (File 985)
***Dialog NewsRoom - 2003 Archive (File 992)
***TRADEMARKSCAN-Czech Republic (File 680)
***TRADEMARKSCAN-Hungary (File 681)
***TRADEMARKSCAN-Poland  (File 682)
                     ***
UPDATING RESUMED
                     ***
RELOADED
***Medline (Files 154-155)
***Population Demographics -(File 581)
***CLAIMS Citation (Files 220-222)
```

REMOVED
***

>>> Enter BEGIN HOMEBASE for Dialog Announcements <<<
>>> of new databases, price changes, etc. <<<
****
KWIC is set to 50.
HILIGHT set on as '*'
*
*
* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED * * *

File 1:ERIC 1966-2004/Mar 11
(c) format only 2004 The Dialog Corporation

Set Items Description
--- ----- -----------
Cost is in DialUnits
?b 155, 5, 73
23mar04 14:36:17 User259876 Session D602.1
$0.31 0.089 DialUnits File1
$0.31 Estimated cost File1
$0.05 TELNET
$0.36 Estimated cost this search
$0.36 Estimated total session cost 0.089 DialUnits

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2004/Mar W2
(c) format only 2004 The Dialog Corp.
***File 155: Medline has been reloaded. Accession numbers***
have changed. Please see HELP NEWS 154 for details.
File 5:Biosis Previews(R) 1969-2004/Mar W2
(c) 2004 BIOSIS
File 73:EMBASE 1974-2004/Mar W2
(c) 2004 Elsevier Science B.V.

Set Items Description
--- ----- -----------
?s (att (w) site?) (s) (integrase or int)
6194 ATT
1827277 SITE?
5707 INTEGRASE
15517 INT
S1 216 (ATT (W) SITE?) (S) (INTEGRASE OR INT)
?s s1 and (attB and attP and attR and attL)
216 S1
574 ATTB
824 ATTP
429 ATTR
265 ATTL
S2 16 S1 AND (ATTB AND ATTP AND ATTR AND ATTL)
?rd
...completed examining records
S3 6 RD (unique items)
?t s3/3,k/all

**3/3,K/1 (Item 1 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

13969026 PMID: 9666077
**Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPVL carrying Panton-Valentine leukocidin genes.**
Kaneko J; Kimura T; Narita S; Tomita T; Kamio Y

Department of Applied Biological Chemistry, Faculty of Agriculture, Tohoku University, Sendai 981-8555, Japan.
Gene (NETHERLANDS) Jul 17 1998, 215 (1) p57-67, ISSN 0378-1119
Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... ATCC 49775). Biosci. Biotechnol. Biochem. 61, 1960-1962). In this study, the complete nucleotide sequence of the phiPVL genome was analyzed, and the att sites (*attL*, *attR*, and *attB*) required for site-specific integration of phiPVL into the host chromosome were also determined. The linear double-stranded phiPVL genome comprised 41401bp with 3' staggered...

... ends (cos) of nine bases and contained 63 ORFs, among which the regulatory proteins involved in DNA replication, structural proteins, a holin, a lysin, an *integrase*, and dUTPase, were tentatively identified by the comparison of the deduced amino acid sequences and by the analysis of the proteins isolated from phiPVL particles. The [lukS-PV-lukF-PV], *attP*, and *int* (*integrase* gene) of phiPVL were all located very close to one another within a 4.0-kb segment on the genome in the order given, and this segment was located at the center from the left and the right cos sites. In addition, the *attP* region contained five direct repeat sequences that showed a high degree of homology with the recombinase-binding sites of some other S. aureus bacteriophages. The...

**3/3,K/2 (Item 2 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


10927020 PMID: 11069650
**Control of directionality in the site-specific recombination system of the Streptomyces phage phiC31.**
Thorpe H M; Wilson S E; Smith M C
Institute of Genetics, University of Nottingham, Queens Medical Centre, Nottingham NG7 2UH, UK.
Molecular microbiology (ENGLAND) Oct 2000, 38 (2) p232-41, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... group of phage integrases related to the resolvase/invertase enzymes. Previously, it was demonstrated that, in an in vitro recombination assay, phiC31 integrase catalyses integration (*attP*/*attB* recombination) but not excision (*attL*/*attR* ). The mechanism responsible for this recombination site selectivity was therefore investigated. Purified integrase was shown to bind with similar apparent binding affinities to between 46 bp and 54 bp of DNA at each of the attachment sites, *attP*, *attB*, *attL* and *attR*. Assays using recombination sites of 50 bp and 51 bp for *attP* and *attB*, respectively, showed that these fragments were functional in *attP*/*attB* recombination and maintained strict site selectivity, i.e. no recombination between non-permissive sites, such as *attP*/*attP*, *attB*/*attL* , etc., was observed. Using bandshifts and supershift assays in which permissive and non-permissive combinations of *att* *sites* were used in the presence of *integrase*, only the *attP*/*attB* combination could generate supershifts. Recombination products were isolated from the supershifted complexes. It was concluded that these supershifted complexes contained the recombination synapse and that...
Chemical Name: *AttR* protein; Bacterial Proteins; Membrane Proteins; Integrases

**3/3,K/3 (Item 3 from file: 155)**

DIALOG(R)File 155:MEDLINE(R)


08920484 PMID: 2046656

**Site-specific recombination in Escherichia coli between the att sites of plasmid pSE211 from Saccharopolyspora erythraea.**

Katz L; Brown D P; Donadio S
Corporate Molecular Biology, Abbott Laboratories, IL 60064.

Molecular & general genetics - MGG (GERMANY) May 1991, 227 (1) p155-9, ISSN 0026-8925 Journal Code: 0125036
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

pSE211 from Saccharopolyspora erythraea integrates site-specifically into the chromosome through conservative recombination between *attP* and *attB* , the plasmid and chromosomal attachment sites. Integration depends on the presence of int, an open reading frame (ORF) that lies adjacent to *attP* and encodes the putative integrase. Immediately upstream of int lies xis (formerly called orf2) which encodes a basic protein that is thought to exhibit DNA binding. xis and int were cloned in various combinations in pUC18 and expressed constitutively in Escherichia coli from the lac promoter. *attP* and *attB* were cloned in Streptomyces or E. coli plasmids containing kanamycin resistance (KmR) or chloramphenicol resistance (CmR) markers. Stable KmR CmR cointegrates formed by *attP* x *attB* or *attP* x *attP* recombination (integration) were obtained in E. coli hosts that expressed int. Co-integrates were not found in hosts expressing int + xis. Excision (intraplasmid *att* *site* recombination) was examined by constructing plasmids carrying *attL* and *attR* or two *attP* sites separating CmR from KmR and by following segregation of the markers in various hosts. Both *attL* x *attR* and *attP* x *attP* excision depended on both xis and *int* in E. coli. pSE211 *att* *site* integration and excision were not affected by a deletion in himA, the gene encoding a subunit of integration host factor.

**3/3,K/4 (Item 4 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


08287396 PMID: 2676729

**Control of prophage integration and excision in bacteriophage P2: nucleotide sequences of the int gene and *att* *sites*.**

Yu A; Bertani L E; Haggard-Ljungquist E
Department of Microbial Genetics, Karolinska Institutet, Stockholm, Sweden.

Gene (NETHERLANDS) Aug 1 1989, 80 (1) p1-11, ISSN 0378-1119 Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Control of prophage integration and excision in bacteriophage P2: nucleotide sequences of the int gene and *att* *sites*.**

Integration of bacteriophage P2 into the Escherichia coli host genome involves recombination between two specific attachment sites, *attP* and *attB* , one on the phage and the other on the host genome, respectively. The reaction is controlled by the product of the phage int gene, a...

...to a prophage [Bertani, Proc. Natl. Acad. Sci. USA 65 (1970) 331-336]. A 1200-bp region of P2 DNA containing the int gene and *attP*, the prophage hybrid ends *attL* and *attR* , and one bacterial attachment site, the preferred site locI from E. coli strain C, have all been sequenced. An open reading frame coding for a...

... amino acids corresponds to the int gene. The gene has no obvious promoter sequence preceding it. The int gene transcript seems to continue past the *attP* site downstream from it, suggesting a possible explanation for the previously observed difference in integration and excision. A comparison of the four attachment sites reveals...

**3/3,K/5 (Item 5 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


08216440 PMID: 2546915
**Nucleotide sequence and expression of the gene for the site-specific integration protein from bacteriophage HP1 of Haemophilus influenzae.**
Goodman S D; Scocca J J
Department of Biochemistry, Johns Hopkins University School of Hygiene and Public Health, Baltimore, Maryland 21205.
Journal of bacteriology (UNITED STATES) Aug 1989, 171 (8) p4232-40, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The nucleotide sequence of the leftmost 2,363 base pairs of the HP1 genome, which includes the attachment site (*attP*) and the integration region, was determined. This sequence contained an open reading frame encoding a 337-residue polypeptide, which is a member of the integrase family of site-specific recombination proteins as judged by sequence comparison. The open reading frame was located immediately adjacent to the *att* *site* and was oriented so that initiation of translation would begin distal to the *att* *site* and end in its immediate vicinity. Expression of this DNA segment in Escherichia coli provided extracts which promoted site-specific recombination between plasmids containing cloned HP1 *attP* and Haemophilus influenzae *attB* sites. This recombination was directional, since no reaction was observed between plasmids containing *attR* and *attL* sites. The reaction was stimulated by the accessory protein integration host factor of E. coli. Evidence was also obtained that the integration host factor influenced the levels of HP1 *integrase* expression. The deduced amino acid sequence of HP1 *integrase* has remarkable similarity to that deduced for the *integrase* of coliphage 186.

**3/3,K/6 (Item 6 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


07399809 PMID: 2951525
**Mutational analysis of integrase arm-type binding sites of bacteriophage lambda. Integration and excision involve distinct interactions of integrase with arm-type sites.**
Bauer C E; Hesse S D; Gumport R I; Gardner J F
Journal of molecular biology (ENGLAND) Dec 5 1986, 192 (3) p513-27, ISSN 0022-2836 Journal Code: 2985088R
Contract/Grant No.: GM07283; GM; NIGMS; GM28717; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Integrative recombination between specific attachment (att) regions of the bacteriophage lambda genome (*attP*) and the Escherichia coli genome ( *attB*) results in a prophage flanked by the hybrid recombinant sites *attL* and *attR* . Each att site contains sequences to which proteins involved in recombination bind. Using site-directed mutagenesis, we have constructed a related set of point mutations within each of the five *Int* "arm-type" binding sites located within *attP*, *attL* and *attR*.

Footprint analyses of binding demonstrate that mutating the arm-type sites significantly disrupts the binding of *Int*. Recombination analyses of mutant *att* *sites* in vivo and in vitro demonstrate that only three wild-type arm-type sites within *attP* are required for efficient integrative recombination. Similar analyses demonstrate that efficient excision can occur with two other different sets of wild-type arm-type sites in *attL* and *attR*. These results demonstrate that integrative and excisive recombination may involve interactions of *Int* with distinct and different subsets of arm-type sites.
?ds

```
Set     Items   Description
S1        216   (ATT (W) SITE?) (S) (INTEGRASE OR INT)
S2         16   S1 AND (ATTB AND ATTP AND ATTR AND ATTL)
S3          6   RD (unique items)
?s s1 and (sequence (w) specific (w) recombination)
             216  S1
         1462804  SEQUENCE
         2515374  SPECIFIC
          117777  RECOMBINATION
              13  SEQUENCE(W)SPECIFIC(W)RECOMBINATION
      S4       0  S1 AND (SEQUENCE (W) SPECIFIC (W) RECOMBINATION)
?s s1 and (recombination)
             216  S1
          117777  RECOMBINATION
      S5     144  S1 AND (RECOMBINATION)
?rd
...examined 50 records  (50)
...examined 50 records  (100)
...completed examining records
      S6      68  RD (unique items)
?s s6 not py>2000
              68  S6
         4831054  PY>2000
      S7      57  S6 NOT PY>2000
?s s7 not s3
              57  S7
               6  S3
      S8      52  S7 NOT S3
?t s8/3,k/all
```

**8/3,K/1 (Item 1 from file: 155)**



14438326 PMID: 10435105

**Minicircle: an improved DNA molecule for in vitro and in vivo gene transfer.**

Darquet A M; Rangara R; Kreiss P; Schwartz B; Naimi S; Delaere P; Crouzet J; Scherman D
UMR 133 CNRS/Rhone-Poulenc Rorer, Vitry sur Seine, France.

Gene therapy (ENGLAND) Feb 1999, 6 (2) p209-18, ISSN 0969-7128
Journal Code: 9421525
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... are thus smaller and potentially safer than the standard plasmids currently used in gene therapy. They were obtained in E. coli by att site-specific *recombination* mediated by the phage lambda *integrase*, which was used to excise the expression cassette from the unwanted plasmid sequences. We produced two minicircles containing the luciferase or beta-galactosidase gene under...

**8/3,K/2 (Item 2 from file: 155)**

DIALOG(R)File 155:MEDLINE(R)


14210782 PMID: 9927749
**The geometry of a synaptic intermediate in a pathway of bacteriophage lambda site-specific *recombination*.**
Cassell G; Moision R; Rabani E; Segall A
Department of Biology and Molecular Biology Institute, San Diego State University, 5500 Campanile Drive, San Diego, CA 92182-4614, USA.
Nucleic acids research (ENGLAND) Feb 15 1999, 27 (4) p1145-51, ISSN 0305-1048 Journal Code: 0411011
Contract/Grant No.: R01-52847; PHS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**The geometry of a synaptic intermediate in a pathway of bacteriophage lambda site-specific *recombination*.**
Bacteriophage lambda uses site-specific *recombination* to move its DNA into and out of the Escherichia coli genome. The *recombination* event is mediated by the phage-encoded integrase (Int) at short DNA sequences known as attachment ( *att* ) *sites*. *Int* catalyzes *recombination* via at least four distinct pathways, distinguishable by their requirements for accessory proteins and by the sequence of their substrates. The simplest *recombination* reaction catalyzed by *Int* does not require any accessory proteins and takes place between two attL sites. This reaction proceeds through an intermediate known as the straight-L bimolecular complex (SL-BMC), a stable complex which contains two attL sites synapsed by *Int*. We have investigated the orientation of the two substrates in the SL-BMC with respect to each other using two independent direct methods, a ligation ...
Descriptors: Bacteriophage lambda--genetics--GE; *DNA, Viral; * *Recombination*, Genetic

**8/3,K/3 (Item 3 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


13776030 PMID: 9472558
**A new DNA vehicle for nonviral gene delivery: supercoiled minicircle.**
Darquet A M; Cameron B; Wils P; Scherman D; Crouzet J
UMR 133 CNRS/Rhone-Poulenc Rorer, Vitry sur Seine, France.
Gene therapy (ENGLAND) Dec 1997, 4 (12) p1341-9, ISSN 0969-7128 Journal Code: 9421525
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... such elements and are consequently safer as they exhibit a high level of biological containment. They are obtained in E. coli by att site-specific *recombination* mediated by the phage lambda *integrase*. The desired eukaryotic expression cassette, bounded by the lambda attP and attB sites was cloned on a recombinant plasmid. The expression cassette was excised in vivo after thermoinduction of the *integrase* gene leading to the formation of two supercoiled molecules the minicircle and the starting plasmid lacking the expression cassette. In various cell lines, purified minicircles...

**8/3,K/4 (Item 4 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


13633234 PMID: 9325107

**Sensing homology at the strand-swapping step in lambda excisive *recombination*.**

Nunes-Duby S E; Yu D; Landy A
Department of Molecular Biology, Cell Biology and Biochemistry, Brown University, Providence, RI 02912, USA.

Journal of molecular biology (ENGLAND) Oct 3 1997, 272 (4) p493-508, ISSN 0022-2836 Journal Code: 2985088R
Contract/Grant No.: AI13544; AI; NIAID; GM33928; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Sensing homology at the strand-swapping step in lambda excisive *recombination*.**

lambda Site-specific *recombination* requires a short stretch of sequence homology that might be sensed during strand swapping, during ligation and/or during isomerization of the obligate Holliday junction...

... and stabilizes the products, as is evident from the different rates of closed Y-junction formation in the presence or absence of homology. Furthermore, under *recombination* conditions, single top-strand-transfers are subject to reversal even in the presence of sequence homology; stability depends on a double-strand-transfer, i.e. dissociation of covalent *Int*. 

Descriptors: Bacteriophage lambda--genetics--GE; **Recombination* , Genetic

**8/3,K/5 (Item 5 from file: 155)**



13523258 PMID: 9209039

**Fis is required for illegitimate *recombination* during formation of lambda bio transducing phage.**

Shanado Y; Kato J; Ikeda H
Department of Molecular Biology, Institute of Medical Science, University of Tokyo, Japan.

Journal of bacteriology (UNITED STATES) Jul 1997, 179 (13) p4239-45, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Fis is required for illegitimate *recombination* during formation of lambda bio transducing phage.**

Specialized transducing particles of phage lambda are formed by illegitimate *recombination* during prophage induction. We examined the effects of an Esherichia coli int, xis, himA, himD, or fis mutation on illegitimate *recombination* during formation of lambda Spi- phage, a class of lambda bio transducing phage. This type of phage is distinguishable from the docL and docR particles...
...higher than that of the wild-type prophage when bacteria were irradiated with UV light. This result indicates that Int and Xis functions, and the *att* *site*, are not required for illegitimate *recombination*. The yield of lambda Spi- phage in the himA, himD, or fis mutant carrying lambda delta *int* -xis prophage was 2.6-, 3.3-, or 17-fold lower, respectively, than that in the wild-type bacteria under UV irradiation. Analysis of the nucleotide sequences of the junctions of the transducing phages indicates that *recombination* at the hotspots, as well as at non-hotspots, takes place between short homologous sequences. Because the growth of infecting phages was not suppressed by the himA, himD, or fis mutation, we conclude that Fis is required, but IHF is only partially required, for short-homology-dependent illegitimate *recombination* during the formation of lambda bio transducing phage.

Descriptors: Bacteriophage lambda--genetics--GE; *Carrier Proteins --genetics--GE; *Escherichia coli Proteins; **Recombination*, Genetic; *Transduction, Genetic

**8/3,K/6 (Item 6 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


13493561 PMID: 9177177
**The catalytic domain of lambda site-specific recombinase.**
Tirumalai R S; Healey E; Landy A
Division of Biology and Medicine, Brown University, Providence, RI 02912, USA.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Jun 10 1997, 94 (12) p6104-9, ISSN 0027-8424 Journal Code: 7505876
Contract/Grant No.: AI13544; AI; NIAID; GM33928; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

...site-specific recombinases. It is a heterobivalent DNA binding protein that makes use of a high energy covalent phosphotyrosine intermediate to catalyze integrative and excisive *recombination* at specific chromosomal sites (*att* *sites*). A 293-amino acid carboxy-terminal fragment of *Int* (C65) has been cloned, characterized, and used to further dissect the protein. From this we have cloned and characterized a 188-amino acid, protease-resistant, carboxy-terminal fragment (C170) that we believe is the minimal catalytically competent domain of *Int*. C170 has topoisomerase activity and converts att suicide substrates to the covalent phosphotyrosine complexes characteristic of *recombination* intermediates. However, it does not show efficient binding to *att* *site* DNA in a native gel shift assay. We propose that lambda *Int* consists of three functional and structural domains: residues 1-64 specify recognition of "arm-type" DNA sequences distant from the region of strand exchange; residues...

... which places Tyr-342 at the center of a 17-amino acid flexible loop. It is proposed that C170 is likely to represent a generic *Int* family domain that thus affords a specific route to studying the chemistry of DNA cleavage and ligation in these recombinases.

**8/3,K/7 (Item 7 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


13349877 PMID: 9023184
**Mutational analysis of protein binding sites involved in formation of the bacteriophage lambda attL complex.**
MacWilliams M; Gumport R I; Gardner J F
Department of Microbiology, University of Illinois at Urbana-Champaign, 61801, USA.
Journal of bacteriology (UNITED STATES) Feb 1997, 179 (4) p1059-67, ISSN 0021-9193 Journal Code: 2985120R
Contract/Grant No.: GM28717; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Bacteriophage lambda site-specific *recombination* requires the formation of higher-order protein-DNA complexes to accomplish synapsis of the partner attachment (att) sites as well as for the regulation of...

... flanking arm regions. The attL site consists of two core sites (C and

C'), an integration host factor (IHF) binding site (H'), and three contiguous *Int* binding arm sites (P'1, P'2, and P'3). In this study, we employed bacteriophage P22 challenge phages to determine which protein binding sites...

... no effect on complex formation. These results support a model in which IHF, bound to the H' site, bends the attL DNA so that the *Int* molecule bound to P'1 also interacts with the C' core site. This bridged complex, along with a second *Int* molecule bound to P'2, helps to stabilize the interaction of a third *Int* with the C core site. The results also indicate that nonspecific DNA binding is a significant component of the *Int*-core interactions and that the cooperativity of *Int* binding can overcome the effects of mutations in the individual arm sites and core sites.

**8/3,K/8 (Item 8 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


12792507 PMID: 7563085
**Single base-pair precision and structural rigidity in a small IHF-induced DNA loop.**
Nunes-Duby S E; Smith-Mungo L I; Landy A
Division of Biology & Medicine, Brown University, Providence, RI 02912, USA.
Journal of molecular biology (ENGLAND) Oct 20 1995, 253 (2) p228-42, ISSN 0022-2836 Journal Code: 2985088R
Contract/Grant No.: AI 13544; AI; NIAID; GM 33928; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... of the H' bend center by a single base-pair to the right or to the left within the very tight loop formed with Lambda *integrase* (*Int*) and IHF in *att*-*site* "intasomes" severely reduces *recombination*. This suggests that a precise, but wrongly positioned, DNA bend within a loop of constant length negatively influences the juxtaposition or "phasing" of the core-type and arm-type *Int* binding sites by differentially affecting the length of each leg of the loop. Furthermore, ten base-pair insertions within this loop that should not interfere with correct helical phasing are sensed in a position-dependent manner. Distal insertions abolish *recombination*, whereas proximal or double insertions (in both legs of the loop) are well tolerated.
...; Base Sequence; Binding Sites; DNA-Binding Proteins--chemistry--CH; Integration Host Factors; Kinetics; Models, Molecular; Molecular Sequence Data; Mutagenesis, Insertional; Plasmids--metabolism--ME; Protein Conformation; *Recombination*, Genetic; Restriction Mapping

**8/3,K/9 (Item 9 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


12623387 PMID: 7743177
**Swapping DNA strands and sensing homology without branch migration in lambda site-specific *recombination*.**
Nunes-Duby S E; Azaro M A; Landy A
Department of Biology and Medicine, Brown University, Providence, Rhode Island 02912, USA.
Current biology - CB (ENGLAND) Feb 1 1995, 5 (2) p139-48, ISSN 0960-9822 Journal Code: 9107782
Contract/Grant No.: AI13544; AI; NIAID; GM-33928; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM

Record type: Completed

**Swapping DNA strands and sensing homology without branch migration in lambda site-specific *recombination*.**

... staggered sites where the two single-strand exchanges occur. We have investigated the validity of such models in the case of bacteriophage lambda site-specific *recombination* . RESULTS: By using synthetic lambda att-site Holliday junctions, incorporating sequence heterologies that impose constraints on branch migration, we have found that the optimal position of the junction for either top-strand or bottom-strand resolution by lambda *integrase* (*Int*) is not at the ends, but close to the middle of the seven base-pair overlap region. A minor shift of the branch point around...

... migration is limited to the central one to three base pairs of the overlap region. They lead to a new model for lambda site-specific *recombination* , in which there are two symmetrical swaps of two to three nucleotides each, linked by a central isomerization step that causes a change of the stacking interactions between the four junction arms. On the basis of isolated strand-joining reactions carried out by *Int* in the presence or absence of base complementarity, we propose that sequence homology is sensed during the annealing step prior to strand joining. The new...

... mechanistic complications associated with large helical rotations required by branch-migration models. CONCLUSIONS: The results reported here suggest that the recognition of sequence homology in *Int*-dependent site-specific *recombination* does not rely primarily on branch migration. The property of cleaving Holliday junctions a few base pairs away from the crossover puts lambda *Int* into the same category as endonucleases that cleave Holliday junctions in homologous *recombination*.

Descriptors: Bacteriophage lambda--genetics--GE; *DNA, Viral--genetics --GE; **Recombination*, Genetic; *Sequence Homology, Nucleic Acid

**8/3,K/10 (Item 10 from file: 155)**



10731397 PMID: 10852483

**Core-binding specificity of bacteriophage integrases.**

Gottfried P; Yagil E; Kolot M

Department of Biochemistry, The George S. Wise Center for Life Sciences, Tel-Aviv University, Israel.

Molecular & general genetics - MGG (GERMANY) May 2000, 263 (4) p619-24, ISSN 0026-8925 Journal Code: 0125036

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The site-specific *recombination* systems of bacteriophages lambda and HK022 share the same mechanism and their integrase proteins show strong homology. Nevertheless the integrase protein of each phage can only catalyze *recombination* between its own *att* *sites*. Previous work has shown that the specificity determinants in the *att* *sites* are located within the sequences that bind the *integrase* to the core of att. DNA fragments that carry attL and attR sites of each phage were challenged with each of the two integrases and the DNA-protein complexes were examined by the gel-retardation technique. The results show that each *integrase* can form higher-order DNA-protein complexes only with its cognate *att* *sites* , suggesting that differences in the mode of binding to the core are responsible for the specificity difference between the two integrases.

...; Proteins--genetics--GE; Bacterial Proteins--metabolism--ME; Bacteriophage lambda--genetics--GE; Cloning, Molecular; DNA Nucleotidyltransferases--genetics--GE; DNA Nucleotidyltransferases --metabolism--ME; Integration Host Factors; Plasmids; *Recombination*,

Genetic; Substrate Specificity

**8/3,K/11 (Item 11 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


10678700 PMID: 10792728
**Specificity determinants for bacteriophage Hong Kong 022 integrase: analysis of mutants with relaxed core-binding specificities.**
Cheng Q; Swalla B M; Beck M; Alcaraz R; Gumport R I; Gardner J F
Department of Microbiology and Biochemistry and College of Medicine, University of Illinois at Urbana-Champaign, IL, 61801, USA.
Molecular microbiology (ENGLAND) Apr 2000, 36 (2) p424-36, ISSN 0950-382X Journal Code: 8712028
Contract/Grant No.: GM 28717; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The integrase (Int) proteins encoded by bacteriophages HK022 and lambda catalyse similar site-specific integration and excision reactions between specific DNA regions known as attachment (*att*) *sites*. However, the *Int* proteins of HK022 and lambda are unable to catalyse *recombination* between non-cognate *att* *sites*. The *att* *sites* of both phages contain weak binding sites for *Int* , known as 'core-type' sites. Negatively acting nucleotide determinants associated with specific core sites (lambda B', HK022 B', HK022 C) are responsible for the barrier to non-cognate *recombination* . In this study, we used challenge phages to demonstrate that the lambda and HK022 Ints cannot bind to core sites containing non-cognate specificity determinants in vivo. We isolated mutants of the HK022 *Int* , which bind the lambda B' core site. Two mutants, D99N and D99A, have changed a residue in the core-binding (CB) domain, which may be...

... a conflicting interaction with the G4 nucleotide of the lambda B' site. We showed that, although our mutants retain the ability to recombine their cognate *att* *sites*, they are unable to recombine lambda *att* *sites*.
...; Bacteriophage lambda--enzymology--EN; Bacteriophage lambda --metabolism--ME; Escherichia coli--virology--VI; Integrases--chemistry--CH ; Molecular Sequence Data; Mutation; Plasmids--genetics--GE; Protein Structure, Secondary; *Recombination*, Genetic; Siphoviridae--genetics--GE

**8/3,K/12 (Item 12 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


10547537 PMID: 10648529
**The amino terminus of bacteriophage lambda integrase is involved in protein-protein interactions during *recombination*.**
Jessop L; Bankhead T; Wong D; Segall A M
Department of Biology and Molecular Biology Institute, San Diego State University, San Diego, California 92182-4614, USA.
Journal of bacteriology (UNITED STATES) Feb 2000, 182 (4) p1024-34, ISSN 0021-9193 Journal Code: 2985120R
Contract/Grant No.: GM52847; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**The amino terminus of bacteriophage lambda integrase is involved in protein-protein interactions during *recombination*.**
Bacteriophage lambda integrase (Int) catalyzes at least four site-specific *recombination* pathways between pairs of attachment (*att*)

*sites*. Protein-protein contacts between monomers of *Int* are presumed to be important for these site-specific *recombination* events for several reasons: *Int* binds to the *att* *sites* cooperatively, catalytic *Int* mutants can complement each other for strand cleavage, and crystal structures for two other recombinases in the *Int* family (Cre from phage P1 and *Int* from Haemophilus influenzae phage HP1) show extensive protein-protein contacts between monomers. We have begun to investigate interactions between *Int* monomers by three approaches. First, using a genetic assay, we show that regions of protein-protein interactions occur throughout *Int* , including in the amino-terminal domain. This domain was previously thought to be important only for high-affinity protein-DNA interactions. Second, we have found that an amino-terminal His tag reduces cooperative binding to DNA. This disruption in cooperativity decreases the stable interaction of *Int* with core sites, where catalysis occurs. Third, using protein-protein cross-linking to investigate the multimerization of *Int* during *recombination*, we show that *Int* predominantly forms dimers, trimers, and tetramers. Moreover, we show that the cysteine at position 25 is present at or near the interface between monomers that is involved in the formation of dimers and tetramers. Our evidence indicates that the amino-terminal domain of *Int* is involved in protein-protein interactions that are likely to be important for *recombination*.

Descriptors: Attachment Sites (Microbiology); *Bacteriophage lambda --genetics--GE; *Integrases--genetics--GE; *Integrases--metabolism--ME; * *Recombination*, Genetic

**8/3,K/13 (Item 13 from file: 155)**



10161017 PMID: 8051182

**Structure of the P22 att site. Conservation and divergence in the lambda motif of recombinogenic complexes.**

Smith-Mungo L; Chan I T; Landy A

Division of Biology and Medicine, Brown University, Providence, Rhode Island 02912.

Journal of biological chemistry (UNITED STATES) Aug 12 1994, 269 (32) p20798-805, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: AI 13544; AI; NIAID; GM 33928; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have defined the bacterial and viral DNA targets (att sites) of P22 site-specific *recombination* and characterized their interaction with *integrase* (*Int* ) protein. The bacterial DNA target, attB, is approximately 27 base pairs and consists of two core type *Int* binding sites as inverted repeats. The top and bottom *Int* cleavage sites fall within the core type *Int* binding sites and are separated by a 7-base pair overlap region. A similar core region is found in the viral DNA target, attP, which is approximately 260 base pairs long and contains two IHF binding sites and five arm type binding sites for *Int*. The results suggest that P22 *Int*, like lambda *Int*, is a heterobivalent DNA-binding protein that is capable of forming complex higher order structures with recombinogenic function. Although P22 and lambda *recombination* involve very similar multiprotein interactions and core region structures, there are significant differences in the arrangements of distal protein binding sites. These differences are discussed in terms of the possible flexibility of the *Int* protein and the specificity with which the higher order complexes assemble and/or function.

**8/3,K/14 (Item 14 from file: 155)**

10160838 PMID: 8051031

**Identification and nucleotide sequence analysis of a transfer-related region in the streptococcal conjugative transposon Tn5252.**

Kilic A O; Vijayakumar M N; al-Khaldi S F

Oklahoma State University, Stillwater 74078.

Journal of bacteriology (UNITED STATES) Aug 1994, 176 (16) p5145-50, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

...of Tn5252 showed two open reading frames, ORF1 and ORF2, adjoining the att site. The organization of this region and the structure of the predicted *integrase* encoded by ORF1 were found to be similar to those of other site-specific *recombination* systems.

**8/3,K/15 (Item 15 from file: 155)**

DIALOG(R)File 155:MEDLINE(R)



10116898 PMID: 8013469

**Dissecting the resolution reaction of lambda integrase using suicide Holliday junction substrates.**

Kho S H; Landy A

Division of Biology and Medicine, Brown University, Providence, RI 02912.

EMBO journal (ENGLAND) Jun 1 1994, 13 (11) p2714-24, ISSN 0261-4189 Journal Code: 8208664

Contract/Grant No.: AI 13544; AI; NIAID; GM 33928; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

... strand exchange between two DNA helices generates the crossed-strand intermediate, or Holliday junction, which is common to many pathways of homologous and site-specific *recombination* . The Int family of recombinases are unique in their ability to both make and resolve Holliday junctions. Previous experiments utilizing 'synthetic' *att* *site* Holliday junctions to study the mechanisms associated with the cleavage, transfer and ligation of DNA strands have been confined to studying reciprocal strand exchanges (a...

... Holliday junctions that make it possible to monitor individual DNA strand cleavage events. These substrates contain a pre-existing nick in the vicinity of the *Int* binding site; when *Int* introduces a second nick into these substrates, the 5'OH nucleophile required for ligation (in either the forward or reverse reaction) is lost by diffusion...

Descriptors: DNA Nucleotidyltransferases--metabolism--ME; *DNA, Viral --metabolism--ME; *Models, Genetic; **Recombination*, Genetic--genetics--GE

**8/3,K/16 (Item 16 from file: 155)**

DIALOG(R)File 155:MEDLINE(R)



09712508 PMID: 8388531

**Sequence requirements for target activity in site-specific *recombination* mediated by the Int protein of transposon Tn 1545.**

Trieu-Cuot P; Poyart-Salmeron C; Carlier C; Courvalin P

Unite des Agents Antibacteriens, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Apr 1993, 8 (1) p179-85, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

**Sequence requirements for target activity in site-specific *recombination* mediated by the Int protein of transposon Tn 1545.**

Excision and integration of Tn1545 occur by reciprocal site-specific *recombination* between 6 (or 7) bp variable sequences present in the recombining attachment (att) sites and designated overlap regions. We devised an assay for Tn1545 transposition in which derivatives containing the cis-acting transposition sequences (attTn 1545) integrate into a target replicon when complemented in trans by the transposon-encoded *integrase* *Int* -Tn. This assay was used to determine the characteristics of the DNA sequence that influence target site selection. Characterization of several integration sites indicated that...

Descriptors: Bacterial Proteins--metabolism--ME; *DNA Nucleotidyltransferases--metabolism--ME; *DNA Transposable Elements; *DNA, Bacterial--genetics--GE; *Escherichia coli--genetics--GE; **Recombination*, Genetic

**8/3,K/17 (Item 17 from file: 155)**



09691994 PMID: 8483447

**SSV1-encoded site-specific *recombination* system in Sulfolobus shibatae.**

Muskhelishvili G; Palm P; Zillig W
Max-Planck-Institut fur Biochemie, Munich, FRG.

Molecular & general genetics - MGG (GERMANY) Mar 1993, 237 (3) p334-42, ISSN 0026-8925 Journal Code: 0125036
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**SSV1-encoded site-specific *recombination* system in Sulfolobus shibatae.**

We present evidence for the existence of a conservative site-specific *recombination* system in Archaea by demonstrating integrative *recombination* of Sulfolobus shibatae virus SSV1 DNA with the host chromosome, catalysed by the SSV1-encoded integrase in vitro. The putative int gene of SSV1 was...

... Escherichia coli yielding a protein of about 39 kDa. This protein alone efficiently recombined linear DNA substrates containing chromosomal (attA) and viral (attP) attachment sites; *recombination* with either negatively or positively supercoiled SSV1 DNA was less efficient. Intermolecular attA x attA and attP x attP *recombination* was also promoted by the SSV integrase. The invariant 44 bp "common attachment core" present in all *att* *sites* contained sufficient information to allow *recombination*, whilst the flanking sequences effected the efficiency. These features clearly distinguish the SSV1--encoded site--specific *recombination* system from others and make it suitable for the study of regulatory mechanisms of SSV1 genome--host chromosome interaction and investigations of the evolution of the *recombination* machinery.

Descriptors: Bacteriophages--genetics--GE; *DNA Nucleotidyltransferases--genetics--GE; **Recombination*, Genetic; *Sulfolobus--genetics--GE

**8/3,K/18 (Item 18 from file: 155)**



08643925 PMID: 2203732

**Interaction of integration host factor from Escherichia coli with the integration region of the Haemophilus influenzae bacteriophage HP1.**

Hwang E S; Scocca J J
Department of Biochemistry, Johns Hopkins University School of Hygiene and Public Health, Baltimore, Maryland 21205.

Journal of bacteriology (UNITED STATES) Sep 1990, 172 (9) p4852-60, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The specific DNA-binding protein integration host factor (IHF) of Escherichia coli stimulates the site-specific *recombination* reaction between the attP site of bacteriophage HP1 and the attB site of its host, Haemophilus influenzae, in vitro and also appears to regulate the expression of HP1 integrase. IHF interacts specifically with DNA segments containing the *att* *sites* and the *integrase* regulatory region, as judged by IHF-dependent retardation of relevant DNA fragments during gel electrophoresis. The locations of the protein-binding sites were identified by...

... two binding sites were present in the vicinity of the attB region, and one region containing three partially overlapping sites was present in the HP1 *integrase* regulatory segment. The binding sites defined in these experiments all contained sequences which matched the consensus IHF binding sequences first identified in the lambda attP...
Descriptors: Bacterial Proteins--metabolism--ME; *Bacteriophages --genetics--GE; *DNA-Binding Proteins--metabolism--ME; *Escherichia coli --genetics--GE; *Haemophilus influenzae--genetics--GE; **Recombination*, Genetic

**8/3,K/19 (Item 19 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


08283893 PMID: 2529039
**Half-att site substrates reveal the homology independence and minimal protein requirements for productive synapsis in lambda excisive *recombination*.**
Nunes-Duby S E; Matsumoto L; Landy A
Division of Biology and Medicine, Brown University, Providence, Rhode Island 02912.
Cell (UNITED STATES) Oct 6 1989, 59 (1) p197-206, ISSN 0092-8674 Journal Code: 0413066
Contract/Grant No.: AI 13544; AI; NIAID; GM 33928; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Half-att site substrates reveal the homology independence and minimal protein requirements for productive synapsis in lambda excisive *recombination*.**
The early events in site-specific excisive *recombination* were studied with phage lambda half-att sites that have no DNA to one side of the strand exchange region; they carry a single core-type *integrase* binding site and either P or P' arm flanking DNA. These half-attR and half-attL sites exhibit normal properties for the initial (covalent) top...

... independent of later steps in the reaction. With these novel substrates we show that Xis specifically promotes the first strand exchange and that attL enhances *Int* cleavage at the top-strand site of attR. It is also shown that synapsis and initial strand transfers do not require DNA-DNA pairing but are mediated by protein-protein and protein-DNA interactions. These involve the two top-strand *Int* binding sites (required for the first strand exchange) and, in addition, one of the two bottom-strand sites (C') responsible for the second strand exchange.
Descriptors: Attachment Sites (Microbiology); *Bacteriophage lambda --genetics--GE; *Base Sequence; *Lysogeny; **Recombination*, Genetic; *Sequence Homology, Nucleic Acid; *Viral Proteins--genetics--GE

**8/3,K/20 (Item 20 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


08257311 PMID: 2672204
**Genome organization in hybrids between prophage phi 80 and Escherichia coli virus phi gamma.**
Gratia J P
Laboratoire de Microbiologie, Faculte de Medecine ULB, Bruxelles.
Research in virology (FRANCE) Jul-Aug 1989, 140 (4) p373-88, ISSN 0923-2516 Journal Code: 8907469
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Prophage phi 80 is used for the detection of "discrete" viruses such as phage phi gamma by genetic *recombination*. Several genetic events have produced a series of hybrids which are currently being characterized. Characteristic genomic properties of the parent phages are recognized in these...

...the origin of the right arm. In both hybrids, the att site is most often a junction point between the parental genomes due to common *int*-promoted *recombination* . New evidence is provided for the formation of viable heterozygous "lambda/gamma"-type bacteriophages.

**8/3,K/21 (Item 21 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


08154496 PMID: 2542933
**Vaccinia DNA topoisomerase I promotes illegitimate *recombination* in Escherichia coli.**
Shuman S
Program in Molecular Biology, Sloan-Kettering Institute, New York, NY 10021.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) May 1989, 86 (10) p3489-93, ISSN 0027-8424 Journal Code: 7505876
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Vaccinia DNA topoisomerase I promotes illegitimate *recombination* in Escherichia coli.**
... nalidixic acid. Restriction analysis of genomic DNA from plaque-purified excisants revealed (in 10 of 10 cases) gross alterations of the DNA structure around the *att* *site* relative to the structure of the parental phage DE3. It is construed therefore that vaccinia DNA topoisomerase I acts to promote illegitimate *recombination* in E. coli.
Descriptors: DNA Topoisomerases, Type I--physiology--PH; *Escherichia coli--genetics--GE; **Recombination*, Genetic; *Vaccinia virus--enzymology --EN

**8/3,K/22 (Item 22 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


07320985 PMID: 3025679
**Deletion of the phage lambda att80 Tn9 genome; the type of intramolecular *recombination*]**
Deletsii genoma faga lambda att80 Tn9; kharakter vnutrimolekuliarnoi rekombinatsii.

Pokrovskaia M S; Karataev G I; Smirnov G B
Molekuliarnaia genetika, mikrobiologiia i virusologiia (USSR) Oct 1986, (10) p33-9, ISSN 0208-0613 Journal Code: 9315607
Document type: Journal Article ; English Abstract
Languages: RUSSIAN
Main Citation Owner: NLM
Record type: Completed

**Deletion of the phage lambda att80 Tn9 genome; the type of intramolecular *recombination*]**

The intramolecular deletion-generating *recombination* which transforms lambda bacteriophage genomes into the plasmids (named pLS) proved to be site-specific to a certain extent. Using electron microscopy heteroduplex analysis three preferential sites for this *recombination* were found in seven independent pLS isolates studied. Att-sites were not registered to be involved in the formation of deletions in isolates studied. It was shown that *recombination* operating in our system was independent of the phage *int* and bacterial recA genes.

Descriptors: Bacteriophage lambda--genetics--GE; *Chromosome Deletion; *DNA Transposable Elements; *Genes, Viral; **Recombination*, Genetic

**8/3,K/23 (Item 23 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06928919 PMID: 2995999

**Generation of single base-pair deletions, insertions, and substitutions by a site-specific *recombination* system.**

Leong J M; Nunes-Duby S E; Landy A
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Oct 1985, 82 (20) p6990-4, ISSN 0027-8424 Journal Code: 7505876
Contract/Grant No.: AI13544; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Generation of single base-pair deletions, insertions, and substitutions by a site-specific *recombination* system.**

The sequence analysis of both products of individual phi 80 site-specific *recombination* events in vivo shows that *recombination* with a secondary attachment (att) site generates several different novel joints at the mismatched position: one *recombination* event resulted in a single base-pair deletion and two other *recombination* events resulted in two different single base-pair substitutions. The characterized products of *recombination* can be straightforwardly interpreted as the outcome of strand exchange involving staggered nicks bracketing the heterology within an overlap region of five to nine base pairs. In comparison, more complex segregation patterns have been observed in previous studies of lambda *recombination* between nonidentical att sites; the nature of the overlap region heterology may have a significant effect on the segregation patterns. To recover both products of a single *recombination* event, we used a plasmid that carries the phi 80 *int* and xis genes and both *att* *sites*. Because the two *att* *sites* are situated in opposite orientation, intramolecular *recombination* between them inverts rather than deletes the intervening segment of DNA. Although subsequent reinversion restores the original gross genetic arrangement, single base-pair insertions, deletions, and substitutions are introduced at the sites of *recombination*. One of the mutations improves the *recombination* efficiency of the secondary *att* *site* and thereby converts a formerly "stable" sequence to an efficient target for rearrangement, and other mutations are predicted to alter the specificity of *recombination*. These pathways may also provide useful models for the efficient generation of localized sequence diversity on a development (as well as evolutionary) time scale.

**8/3,K/24 (Item 24 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06747851 PMID: 3156374
**Interaction of the lambda site-specific *recombination* protein Xis with attachment site DNA.**
Yin S; Bushman W; Landy A
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Feb 1985, 82 (4) p1040-4, ISSN 0027-8424
Journal Code: 7505876
Contract/Grant No.: AI13544; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Interaction of the lambda site-specific *recombination* protein Xis with attachment site DNA.**
...surface of) the bound Xis protein. The Xis binding data presented here establishes that Xis, like the other two proteins involved in lambda site-specific *recombination* , interacts specifically with att DNA. This rules out that class of models in which the profound effects of Xis on the directionality of site-specific *recombination* are mediated solely through protein-protein interactions or modification of another protein. In addition, nuclease protection experiments with pairwise combinations of the proteins show that Xis and integration host factor (IHF), or Xis and *Int*, can bind simultaneously to either the phage or right prophage *att* *sites* , and the DNA sequences protected are the sum of those protected with each protein alone. It is therefore unlikely that the effect of Xis on the direction of *recombination* is exerted by directly blocking the binding of *Int* or IHF to one or more of their respective binding sites.
; Bacterial Proteins--metabolism--ME; Bacteriophage lambda--genetics--GE; Base Sequence; Binding Sites; DNA, Viral--genetics--GE; Integrases; Integration Host Factors; *Recombination*, Genetic; Repetitive Sequences, Nucleic Acid

**8/3,K/25 (Item 25 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06647130 PMID: 6092961
**Resolution of synthetic att-site Holliday structures by the *integrase* protein of bacteriophage lambda.**
Hsu P L; Landy A
Nature (ENGLAND) Oct 25-31 1984, 311 (5988) p721-6, ISSN 0028-0836
Journal Code: 0410462
Contract/Grant No.: AI13544; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Resolution of synthetic att-site Holliday structures by the *integrase* protein of bacteriophage lambda.**
Site-specific *recombination* of the bacteriophage lambda genome into and out of the host bacterial genome is postulated to involve the formation of Holliday structure intermediates by reciprocal single-strand exchanges. Synthetic analogues of the predicted *recombination* intermediates are resolved in vitro by the protein product of the lambda int gene. Some of the structural features and reaction conditions for this genetic *recombination* can now be defined.
Descriptors: Bacteriophage lambda--genetics--GE; *DNA Transposable Elements; *Escherichia coli--genetics--GE; *Genes, Bacterial; *Genes,

Synthetic; *Genes, Viral; **Recombination*, Genetic; *Viral Proteins --metabolism--ME

**8/3,K/26 (Item 26 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06377662 PMID: 6235918
**Patterns of lambda Int recognition in the regions of strand exchange.**
Ross W; Landy A
Cell (UNITED STATES) May 1983, 33 (1) p261-72, ISSN 0092-8674 Journal Code: 0413066
Contract/Grant No.: 5 T32 GM 07601; GM; NIGMS; AI 13544; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Int protein has two classes of binding sites within the phage *att* *site* : the arm-type recognition sequences are found in three specific sites that are distant from the region of strand exchange; the junction-type recognition sequences occur as inverted pairs around the crossover region in both attP and attB. During *recombination* between attP and attB each of the four DNA strands is cut at a homologous position within each of the junction-type *Int* binding sites. In all four junction-type sites *Int* protein interacts primarily with the same face of the DNA helix, as determined by those purine nitrogens that are protected against methylation by dimethylsulfate. Efficient...
... type binding sites. In addition, the sequence between, but not part of, the two junction-type sites (the overlap region) is strongly conserved in secondary *att* *sites*. Thus, in the vicinity of strand exchange, attP and a recombining partner, such as attB, are very similar; each comprises two junction-type *Int* recognition sites and an overlap (crossover) region.
Descriptors: Bacteriophage lambda--genetics--GE; *DNA, Viral--genetics --GE; *Lysogeny; **Recombination*, Genetic

**8/3,K/27 (Item 27 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06320359 PMID: 6317202
**The mechanism of phage lambda site-specific *recombination* : site-specific breakage of DNA by Int topoisomerase.**
Craig N L; Nash H A
Cell (UNITED STATES) Dec 1983, 35 (3 Pt 2) p795-803, ISSN 0092-8674 Journal Code: 0413066
Contract/Grant No.: GM07498; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**The mechanism of phage lambda site-specific *recombination* : site-specific breakage of DNA by Int topoisomerase.**
... other breakage product has a 5' OH terminus. Int is the first procaryotic topoisomerase shown to break DNA in this manner. We find that in *att* *sites*, *Int* breaks DNA within the 15 bp homologous core. These sites of *Int* topoisomerase action result from the interaction of *Int* with "junction-type" recognition sequences (CAACTTNNT), and *Int* topoisomerase acts between the 7th and 8th bases of this sequence. The sites of breakage within the cores of attP and attB coincide exactly with positions where breakage and reunion occur during *Int*-dependent *recombination*. These results indicate that *Int* topoisomerase executes strand exchange during *recombination*.
Descriptors: Bacteriophage lambda--genetics--GE; *DNA Helicases

--physiology--PH; **Recombination*, Genetic

**8/3,K/28 (Item 28 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06306580 PMID: 6358802
**Properties and products of the cloned int gene of bacteriophage P2.**
Ljungquist E; Bertani L E
Molecular & general genetics - MGG (GERMANY, WEST) 1983, 192 (1-2) p87-94, ISSN 0026-8925 Journal Code: 0125036
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... fragment, which has its endpoints within phage genes T and C, carries the structural P2 int gene as well as its promoter and the phage *att* *site*. When introduced into a suitable bacterial host, the cloned fragment mediates the integration and excision of *int*- mutants of P2 and *recombination* within the phage *att* *site* in mixed infection. All these activities are independent of the orientation of the fragment within the plasmid. When introduced into minicells, the fragment produces, in addition to the products of genes D and U, a protein of 35-37,000 daltons identified as the *int* protein. A study of the map location of two amber *int* mutants, together with the sizes of the polypeptides they produce, indicates that the P2 *int* gene is transcribed from right to left on the P2 map, i.e. starting near gene C and proceeding toward att.
; Chromosome Mapping; Cloning, Molecular; DNA, Viral--genetics--GE; Escherichia coli--genetics--GE; Genetic Markers; Lysogeny; Mutation; Plasmids; *Recombination*, Genetic; Viral Proteins--genetics--GE

**8/3,K/29 (Item 29 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


06073678 PMID: 6962313
**Genetic map of coliphage 186 from a novel use of marker rescue frequencies.**
Hocking S M; Egan J B
Molecular & general genetics - MGG (GERMANY, WEST) 1982, 187 (1) p87-95, ISSN 0026-8925 Journal Code: 0125036
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... phage 186 has been constructed, using the frequency of marker rescue from 186 mutant prophages for genes to the left of att, and int promoted *recombination* for genes to its right. At the left end of the genome lie 7 genes involved in the formation of the phage head, followed to...

... the late control gene, lies to the right of this group but to the left of the phage attachment site. To the right of the *att* *site* lie the non-essential genes (cI and cII) involved in lysogen formation and the gene (A) required for 186 DNA synthesis.
; Alleles; Gene Frequency; Genetic Markers; Mutation; *Recombination*, Genetic

**8/3,K/30 (Item 30 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05837766 PMID: 6281134

**Phasmids: hybrids between ColE1 plasmids and E. coli bacteriophage lambda.**
Brenner S; Cesareni G; Karn J
Gene (NETHERLANDS) Jan 1982, 17 (1) p27-44, ISSN 0378-1119 Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Plasmids carrying cloned lambda att sites may be integrated into the bacteriophage genome by the site-specific *recombination* mechanism of lambda. The cross, referred to as "lifting" the plasmid, requires mixed infection of an Escherichia coli strain carrying the plasmid with two appropriately...

... more plasmids. We call these recombinants phasmids. They contain multiple att sites introduced at the ends of the integrated plasmids, and in the presence of *integrase*, *recombination* between these *att* *sites* can be exploited to effect release of the plasmid components. These novel genetic elements can be used in a variety of ways as vectors in...
Descriptors: Attachment Sites (Microbiology); *Bacteriophage lambda --genetics--GE; *Lysogeny; *Plasmids; **Recombination*, Genetic

**8/3,K/31 (Item 31 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05700289 PMID: 6457725
**Structure and function of the phage lambda att site: size, *int*-binding sites, and location of the crossover point.**
Mizuuchi K; Weisberg R; Enquist L; Mizuuchi M; Buraczynska M; Foeller C; Hsu P L; Ross W; Landy A
Cold Spring Harbor symposia on quantitative biology (UNITED STATES) 1981, 45 Pt 1 p429-37, ISSN 0091-7451 Journal Code: 1256107
Contract/Grant No.: AI-13544; AI; NIAID; GM-07046; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Structure and function of the phage lambda att site: size, *int*-binding sites, and location of the crossover point.**
Descriptors: Attachment Sites (Microbiology); *Bacteriophage lambda --genetics--GE; *Escherichia coli--genetics--GE; *Lysogeny; * *Recombination*, Genetic

**8/3,K/32 (Item 32 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05584696 PMID: 6263855
**Secondary lambda attachment site in the threonine operon attenuator of Escherichia coli.**
Chapman J; Gardner J F
Journal of bacteriology (UNITED STATES) Jun 1981, 146 (3) p1046-54, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

... initiated at a gamma promoter, are terminated efficiently at the thr attenuator. It is also possible that this prophage att site is able to undergo *int* dependent site-specific *recombination* which with another

nearby secondary *att* *site*. Evidence is also presented which suggests that a base or sequence to the left of position -6 in the core is necessary fo excisive *recombination*.

**8/3,K/33 (Item 33 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05431064 PMID: 7435807

**Site-specific *recombination* in bacteriophage lambda: structural analyses of reactive DNA sequences.**

Landy A; Hsu P L; Ross W; Buraczynska M

American journal of tropical medicine and hygiene (UNITED STATES) Sep 1980, 29 (5 Suppl) p1099-106, ISSN 0002-9637 Journal Code: 0370507
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Site-specific *recombination* in bacteriophage lambda: structural analyses of reactive DNA sequences.**

Site-specific integrative *recombination* in bacteriophage lambda involves unequal partners. The minimal phage att site is composed of approximately 240 base pairs and has four distinct *Int* binding sites that differ in size and response to heparin challenge. There appear to be two size classes of *Int* binding sites, approximately 30-35 base pairs and 15 base pairs. The sites at the common core and in the P' arm are of the...

... Two sites in the P arm are of the latter class. Thus far, three of the four sites have been shown to be necessary for *att* *site* function. In contrast, the minimal sequence required for a phage *att* *site* partner (such as the bacterial *att* *site*) may not be much larger than the 15 base pair common core. We have suggested a model in which integrative *recombination* involves two unequal partners; accordingly the phage *att* *site* is referred to as the "donor" and the bacterial *att* *site*, or its analogue, is referred to as the "recipient."

Descriptors: Bacteriophages--genetics--GE; **Recombination*, Genetic

**8/3,K/34 (Item 34 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05374621 PMID: 6447585

**Int-protein lambda phage DNA binding site is situated to the right of the *att*-*site*]**

Mesto sviazyvaniia int-belka s DNK faga lambda raspolozheno sprava ot att-saita.

Kravchenko V V; Vasilenko S K; Gileva I P

Doklady Akademii nauk SSSR (USSR) 1980, 252 (5) p1255-7, ISSN 0002-3264 Journal Code: 7505465
Document type: Journal Article
Languages: RUSSIAN
Main Citation Owner: NLM
Record type: Completed

**Int-protein lambda phage DNA binding site is situated to the right of the *att*-*site*]**

; Binding Sites; *Recombination*, Genetic

**8/3,K/35 (Item 35 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


05294907 PMID: 6246439

**The lambda phage att site: functional limits and interaction with *Int* protein.**
Hsu P L; Ross W; Landy A
Nature (ENGLAND) May 8 1980, 285 (5760) p85-91, ISSN 0028-0836
Journal Code: 0410462
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**The lambda phage att site: functional limits and interaction with *Int* protein.**
Site specific integrative *recombination* of bacteriophage lambda involves unequal partners. The minimal phage att site is composed of approximately 240-base pairs and four distinct binding sites for *Int* protein, at least three of which are crucial for function. This 'donor site' recombines efficiently with a smaller 'recipient site' that lacks the extensive interactions with *Int* protein.

**8/3,K/36 (Item 36 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


04931281 PMID: 364480
**Structure of the lambda att sites generated by *int*-dependent deletions.**
Hoess R H; Landy A
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Nov 1978, 75 (11) p5437-41, ISSN 0027-8424
Journal Code: 7505876
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

**Structure of the lambda att sites generated by *int*-dependent deletions.**
Bacteriophage lambda integrates into the chromosome of its Escherichia coli host by means of a site-specific *recombination* between a locus on the phage chromosome (phage att site) and a locus on the bacterial chromosome (bacterial att site). The nucleotide sequence of four lambda att sites altered in site-specific *recombination* has been determined. The *int*-dependent deletions that generated these *att* *sites* have one end point within the phage *att* *site* and extend either to the left or to the right. As a result of the new internucleotide bond created by deletion formation, these phage have alterations in the 15-base-pair common core region. The new DNA sequences brought to the *att* *sites* by the deletions, designated delta for regions to the left and delta' for regions to the right, do not share any discernible homology with their analogous counterparts in the phage *att* *site* arms, P and P', respectively, or with the bacterial *att* *site* arms, B and B', respectively. The finding of alterations in the 15-base-pair common core region necessitates a reinterpretation of the genetic properties of these *att* *sites* in site-specific *recombination*. The structure of these sites in relation to their genetic properties can be viewed as being consistent with a model in which the only specificity elements in *int*-dependent site-specific *recombination* are the common core region, O, and the phage arms, P and P'.
; Base Sequence; Chromosomes, Bacterial; Coliphages--metabolism--ME; DNA Restriction Enzymes; Escherichia coli--metabolism--ME; Oligodeoxyribonucleotides--metabolism--ME; *Recombination*, Genetic

**8/3,K/37 (Item 37 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)


04630471 PMID: 334634

**Site-specific *recombination* between phages lambda and phi 81 and integration of hybrid phages lambda-phi 81]**
Izuchenie sait-spetsificheskoi rekombinatsii mezhdu fagami liambda i fi 81 i integratsii gibridnykh fagov liambda-fi 81.
Balandina L a; Sineokii S P; Krylov V N
Genetika (USSR) 1977, 13 (8) p1441-5, ISSN 0016-6758
Journal Code: 0047354
Document type: Journal Article ; English Abstract
Languages: RUSSIAN
Main Citation Owner: NLM
Record type: Completed

**Site-specific *recombination* between phages lambda and phi 81 and integration of hybrid phages lambda-phi 81]**
Dependence of the formation frequency of hybrid phages immlambdahphi81 and immphi81hlambda in *recombination* between phages lambda and phi81 from int-function of both phages is studied. Phages with hybrid *att*-*sites* (Plambda OP'phi81 and Pphi81OP'lambda) are isolated and the efficiency of integration of these phages into bacterial chromosome is determined.
Descriptors: Coliphages--genetics--GE; *Genes, Viral; *Hybridization, Genetic; **Recombination*, Genetic

**8/3,K/38 (Item 1 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0008839745 BIOSIS NO.: 199396004161
**SSV1-encoded site-specific *recombination* system in Sulfolobus shibatae**
AUTHOR: Mushelishvili Georgi (Reprint); Palm Peter; Zillig Wolfram
AUTHOR ADDRESS: Max-Planck-Inst. Biochemie, W-8033 Martinsried, Munich, Germany**Germany
JOURNAL: Molecular and General Genetics 237 (3): p334-342 1993
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

**SSV1-encoded site-specific *recombination* system in Sulfolobus shibatae**

ABSTRACT: We present evidence for the existence of a conservative site-specific *recombination* system in Archaea by demonstrating integrative *recombination* of Sulfolobus shibatae virus SSV1 DNA with the host chromosome, catalysed by the SSV1-encoded integrase in vitro. The putative int gene of SSV1 was...

...Escherichia coli yielding a protein of about 39 kDa. This protein alone efficiently recombined linear DNA substrates containing chromosomal (attA) and viral (attP) attachment sites; *recombination* with either negatively or positively supercoiled SSV1 DNA was less efficient. Intermolecular attA times attA and attP times attP *recombination* was also promoted by the SSV integrase. The invariant 44bp "common attachment core" present in all *att* *sites* contained sufficient information to allow *recombination*, whilst the flanking sequences effected the efficiency. These features clearly distinguish the SSV1 - encoded site - specific *recombination* system from others and make it suitable for the study of regulatory mechanisms of SSV1 genome - host chromosome interaction and investigations of the evolution of the *recombination* machinery.
DESCRIPTORS:
MISCELLANEOUS TERMS: ...CONSERVATIVE SITE-SPECIFIC *RECOMBINATION* SYSTEM...

...*RECOMBINATION* MACHINERY EVOLUTION

**8/3,K/39 (Item 2 from file: 5)**

DIALOG(R)File 5:Biosis Previews(R)


0007024778 BIOSIS NO.: 199039078167
**FEATURES OF INT-MEDIATED RESOLUTION OF HOLLIDAY JUNCTIONS DERIVED FROM LAMBDA-*ATT* *SITE* DNA**
**BOOK TITLE: SARMA, R. H. AND M. H. SARMA (ED.). STRUCTURE AND METHODS, VOL. 1. HUMAN GENOME INITIATIVE AND DNA *RECOMBINATION*; PROCEEDINGS OF THE SIXTH CONVERSATION IN THE DISCIPLINE BIOMOLECULAR STEREODYNAMICS, ALBANY, NEW YORK, USA, JUNE 6-10, 1989. IX+251P. ADENINE PRESS: SCHENECTADY, NEW YORK, USA. ILLUS**
AUTHOR: FRANZ B (Reprint); LANDY A
AUTHOR ADDRESS: DIV BIOL MED, BROWN UNIV, PROVIDENCE, RI 02912, USA**USA
p183-192 1990
ISBN: 0-940030-29-2
DOCUMENT TYPE: Book; Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

**FEATURES OF INT-MEDIATED RESOLUTION OF HOLLIDAY JUNCTIONS DERIVED FROM LAMBDA-*ATT* *SITE* DNA**
**BOOK TITLE: SARMA, R. H. AND M. H. SARMA (ED.). STRUCTURE AND METHODS, VOL. 1. HUMAN GENOME INITIATIVE AND DNA *RECOMBINATION*; PROCEEDINGS OF THE SIXTH CONVERSATION IN THE DISCIPLINE BIOMOLECULAR STEREODYNAMICS, ALBANY, NEW YORK, USA, JUNE 6-10, 1989. IX+251P. ADENINE PRESS: SCHENECTADY, NEW YORK...**

**8/3,K/40 (Item 3 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0005670615 BIOSIS NO.: 198784024764
**DELETIONS IN BACTERIOPHAGE LAMBDA-ATT80 TN-9 GENOME NATURE OF INTRAMOLECULAR *RECOMBINATION***
AUTHOR: POKROVSKAYA M S (Reprint); KARATAEV G I; SMIRNOV G B
AUTHOR ADDRESS: NF GAMALEYA RES INST EPIDEMIOL MICROBIOL, ACAD MED SCI USSR, MOSCOW, USSR**USSR
JOURNAL: Molekulyarnaya Genetika Mikrobiologiya i Virusologiya (10): p33-39 1986
ISSN: 0208-0613
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

**DELETIONS IN BACTERIOPHAGE LAMBDA-ATT80 TN-9 GENOME NATURE OF INTRAMOLECULAR *RECOMBINATION***

ABSTRACT: The intramolecular deletion-generating *recombination* which transforms .lambda. bacteriophage genomes into the plasmids (named pLS) proved to be site-specific to a certain extent. Using electron microscopy heteroduplex analysis three preferential sites for this *recombination* were found in seven independent pLS isolates studied. Att-sites were not registered to be involved in the formation of deletions in isolates studied. It was shown that *recombination* operating in our system was independent of the phage *int* and bacterial recA genes.

**8/3,K/41 (Item 4 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0005098313 BIOSIS NO.: 198681062204
**ON THE SITE SPECIFIC *RECOMBINATION* OF PHAGE 16-3 OF RHIZOBIUM-MELILOTI IDENTIFICATION OF GENETIC ELEMENTS AND ATT RECOMBINATIONS**
AUTHOR: OLASZ F (Reprint); DORGAI L; PAPP P; HERMESZ E; KOSA E; OROSZ L
AUTHOR ADDRESS: DEP GENETICS, ATTILA JOZSEF UNIV, KOZEPFASOR 52, H-6726

SZEGED, HUNGARY**HUNGARY
JOURNAL: Molecular and General Genetics 201 (2): p289-295 1985
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**ON THE SITE SPECIFIC *RECOMBINATION* OF PHAGE 16-3 OF RHIZOBIUM-MELILOTI IDENTIFICATION OF GENETIC ELEMENTS AND ATT RECOMBINATIONS**

...ABSTRACT: xis, responsible for integration and excision of phage 16-3, have been identified and cloned. Mutants were isolated, permitting the investigation of int, xis and *att* *sites* (attP, attR, attB) in trans arrangements. The efficiency and role of *int*- and xis-promoted reactions and of homologous *recombination* in thr formation of lysogenic cells are established. The possible use of the cloned *int*-attP chromosomal segment in the manipulation of Rhizobium meliloti is discussed.

**8/3,K/42 (Item 5 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0003818863 BIOSIS NO.: 198375002806
**BIOCHEMICAL ANALYSIS OF ATT DEFECTIVE MUTANTS OF THE PHAGE LAMBDA SITE SPECIFIC *RECOMBINATION* SYSTEM**
AUTHOR: ROSS W (Reprint); SHULMAN M; LANDY A
AUTHOR ADDRESS: DIV BIOL AND MED, BROWN UNIV, PROVIDENCE, RI 02912, USA** USA
JOURNAL: Journal of Molecular Biology 156 (3): p505-530 1982
ISSN: 0022-2836
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**BIOCHEMICAL ANALYSIS OF ATT DEFECTIVE MUTANTS OF THE PHAGE LAMBDA SITE SPECIFIC *RECOMBINATION* SYSTEM**

...ABSTRACT: residues within the 15 base-pair core, the region of homology between the recombining sites. As judged by DNase I protection experiments, binding of the *Int* protein is the same in the mutant and wild-type core sites. A difference in the *Int* binding to mutant cores is observed when the small neocarzinostatin molecule is used as a nuclease probe. The differences between mutant and wild type lead to the suggestion that *Int* is interacting with sequences at the core-arm junctions. Accordingly, the mutants are proposed to be defective in the spacing of *Int* monomers bound at 2 recognition sequences spanning the core-arm junctions. The anomalous electrophoretic mobility of wild-type att fragments and, more specifically, the effect of the single base core deletion on electrophoretic mobility are discussed. The mutant att2501, defective in att and *int* functions, was sequenced and found to be a 335 base-pair deletion removing the coding region for 25 amino acids from the carboxy-terminal end of *Int* and the entire *att* *site*. The postulated origin of the 501 mutation is also consistent with the model of 2 juxtaposed *Int* recognition sites. [Escherichia coli was used.]....

**8/3,K/43 (Item 6 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0003630102 BIOSIS NO.: 198274046525
**PHASMIDS HYBRIDS BETWEEN COL-E-1 PLASMIDS AND ESCHERICHIA-COLI BACTERIO PHAGE LAMBDA**
AUTHOR: BRENNER S (Reprint); CESARENI G; KARN J
AUTHOR ADDRESS: MED RES COUNC LAB MOL BIOL, HILLS RD, CAMBRIDGE CB2 2QH, UK

**UK
JOURNAL: Gene (Amsterdam) 17 (1): p27-44 1982
ISSN: 0378-1119
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Plasmids carrying cloned phage .lambda. att sites may be integrated into the bacteriophage genome by the site-specific *recombination* mechanism of .lambda.. The cross, referred to as lifting the plasmid, requires mixed infection of an E. coli strain carrying the plasmid with 2 appropriately...

...more plasmids. These recombinants are called phasmids. They contain multiple att sites introduced at the ends of the integrated plasmids, and in the presence of *integrase*, *recombination* between these *att* *sites* can be exploited to effect release of the plasmid components. These novel genetic elements can be used in a variety of ways as vectors in...
DESCRIPTORS: CLONING VECTOR ATT SITE *INTEGRASE* RECOMBINANT DNA

**8/3,K/44 (Item 7 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0003439680 BIOSIS NO.: 198223013615
**SITE SPECIFIC *RECOMBINATION* IN BACTERIO PHAGE P-2**
AUTHOR: BERTANI L E (Reprint); LJUNGQUIST E; BERTANI G
AUTHOR ADDRESS: MICROBIAL GENETICS LABORATORY, KAROLINSKA INSTITUTET, 104 01 STOCKHOLM, SWEDEN**SWEDEN
JOURNAL: Microbiology (Washington D C) p61-63 1981
CONFERENCE/MEETING: SEMINAR AT THE ANNUAL MEETING FOR THE AMERICAN SOCIETY OF MICROBIOLOGY, MIAMI BEACH, FLA., USA, MAY 11-16, 1980. MICROBIOLOGY (WASH D C).
ISSN: 0098-1540
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

**SITE SPECIFIC *RECOMBINATION* IN BACTERIO PHAGE P-2**
DESCRIPTORS: ATT SITE *INT* GENE PRODUCT COX II GENE OLD GENE MUTATION

**8/3,K/45 (Item 8 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0003039586 BIOSIS NO.: 198070071073
**INT-H AN INT MUTATION OF PHAGE LAMBDA THAT ENHANCES SITE SPECIFIC *RECOMBINATION***
AUTHOR: MILLER H I (Reprint); MOZOLA M A; FRIEDMAN D I
AUTHOR ADDRESS: DEP MOL BIOL, UNIV CALIF, BERKELEY, CALIF 94720, USA**USA
JOURNAL: Cell 20 (3): p721-730 1980
ISSN: 0092-8674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**INT-H AN INT MUTATION OF PHAGE LAMBDA THAT ENHANCES SITE SPECIFIC *RECOMBINATION***

...ABSTRACT: coliphage .lambda. and results in the synthesis of an integrase with enhanced activity; this result is manifested by an ability to support .lambda. site-specific *recombination* relatively efficiently, under conditions where the wild-type integrase functions inefficiently. The level of site-specific *recombination* seen in the presence of the

int+ integrase in himA- hosts is greatly reduced, as measured by lysogen formation, intramolecular site-specific integration and excision...
...high levels of activities under these conditions. Int-h3 is also more active in other host mutants (himB and hip) that reduce .lambda. site-specific *recombination*. In the absence of the normal attB site, the frequency of lysogen formation (at secondary sites) by .lambda. int+ is reduced 200-fold. Although .lambda...

...in attB-deleted hosts. .lambda. int-h3 requires himA function for integration at secondary sites. The fact that the int-h3 integrase uses the same *att* *sites* and the same host functions as the *int*+ *integrase* suggests that the mutation results in a quantitative, rather than a qualitative change in *integrase* activity; that is, the *int*-h3 *integrase* is more active. The mutant *integrase* supports site-specific *recombination* with *att* *sites* that carry the att24 mutation. The *int*-h3 *integrase* is apparently endowed with an enhanced ability to recognize att sequences, including some that are not effectively recognized by wild-type *integrase*.

**8/3,K/46 (Item 9 from file: 5)**



0003019137 BIOSIS NO.: 198070050624

**SITE SPECIFIC *RECOMBINATION* FUNCTIONS OF BACTERIO PHAGE LAMBDA DNA SEQUENCE OF REGULATORY REGIONS AND OVERLAPPING STRUCTURAL GENES FOR INT AND XIS PROTEINS**

AUTHOR: HOESS R H (Reprint); BIDWELL K; LANDY A; FOELLER C
AUTHOR ADDRESS: DIV BIOL MED, BROWN UNIV, PROVIDENCE, RI 02912, USA**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 77 (5): p2482-2486 1980
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**SITE SPECIFIC *RECOMBINATION* FUNCTIONS OF BACTERIO PHAGE LAMBDA DNA SEQUENCE OF REGULATORY REGIONS AND OVERLAPPING STRUCTURAL GENES FOR INT AND XIS PROTEINS**

ABSTRACT: Site-specific *recombination* in bacteriophage .lambda. is mediated by 2 phage-encoded proteins, Int and Xis. The structural genes encoding these proteins are located immediately to the right of their site of action, the phage *att* *site*. The DNA sequence for both the structural and regulatory regions of these genes was determined. The location and reading frame of the xis gene were...

...a MW of 8630; it is rich in basic amino acids with lysine and arginine comprising 25% of the 72 amino acids. Identification of the *int* reading frame was also unambiguous. From the DNA sequence, *Int* has a MW of 40,330; of the 356 amino acids, 69 are basic and 46 are acidic. In the NH2-terminal portion of *Int*, 35% of the first 20 amino acids are basic. The site-specific *recombination* functions form a very tight cluster (att-*int*-xis) on the .lambda. chromosome. The combined protein-encoding sequences of xis and *int* start 1347 base pairs, and terminate 84 base pairs, from the center of the phage *att* *site*. The 2 genes overlap one another by 20 base pairs (xis is upstream of *int*) and a possible means of controlling the relative synthesis rates of *Int* and Xis at the level of translation is proposed. Control at the level of transcription is also considered. The mutation intc226 leads to constitutive production of *Int*, independent of cII/cIII activator proteins normally required for transcription from the pI promoter. This mutation is the result of a single base change (in...

**8/3,K/47 (Item 10 from file: 5)**

DIALOG(R)File 5:Biosis Previews(R)


0002984727 BIOSIS NO.: 198070016214
**INTEGRATION AND EXCISION OF TRANSDUCING BACTERIO PHAGES CARRYING THE RPO-B AND RPO-C GENES OF ESCHERICHIA-COLI RNA POLYMERASE**
AUTHOR: MINDLIN S Z (Reprint); KHOLODII G YA; KOVALEV YU N; KIVER I F
AUTHOR ADDRESS: INST MOL GENET, ACAD SCI USSR, MOSCOW, USSR**USSR
JOURNAL: Genetika 15 (10): p1756-1766 1979
ISSN: 0016-6758
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

...ABSTRACT: vphi.80, imm.lambda.) from the locus bfe of E. coli K-12 and incorporating the adjacent region of chromosome rrnB-rpoB were studied. Hybrid *att*-*sites* of rifd phages (.DELTA.op') are different in their structure due to the insertion of the parental .lambda. and .lambda.att80 phages into different sites...

...to be due to the incorporation of a region of bacterial chromosome rrnB-rpoB into phage genome and depend upon the functioning of an unidentified *int*-independent system of *recombination*.
DESCRIPTORS: PHAGE LAMBDA PHAGE PHI-80 *RECOMBINATION*

**8/3,K/48 (Item 11 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0002888339 BIOSIS NO.: 198069002326
**STRUCTURAL FEATURES OF PHAGE LAMBDA SITE SPECIFIC *RECOMBINATION* AT A SECONDARY ATT SITE IN GALT**
AUTHOR: BIDWELL K (Reprint); LANDY A
AUTHOR ADDRESS: SECT MICROBIOL MOL BIOL, DIV BIOL MED, BROWN UNIV, PROVIDENCE, RI 02912, USA**USA
JOURNAL: Cell 16 (2): p397-406 1979
ISSN: 0092-8674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**STRUCTURAL FEATURES OF PHAGE LAMBDA SITE SPECIFIC *RECOMBINATION* AT A SECONDARY ATT SITE IN GALT**

ABSTRACT: Integration of bacteriophage .lambda. DNA into the chromosome of its Escherichia coli host proceeds via a site-specific *recombination* between specific loci (att sites) on the phage and bacterial chromosomes. Infection of an E. coli host deleted for the primary bacterial att site results...
...sequence analysis of such a secondary att site, that occurring in the galT gene, is reported here, and several features pertinent to the mechanism of *int*-dependent site-specific *recombination* are discussed. Previous studies showed that the crossover in *int*-dependent *recombination* must be somewhere within a 15 bp [base pairs] sequence (core region) common to the phage and primary bacterial *att* *sites*, and to the left and right prophage *att* *sites* which are at the junctures between prophage and host DNA. Comparison of the galT secondary prophage *att* *sites* with the primary prophage *att* *sites* allows determination of the analogous core region in the galT secondary *att* *site*. The 15 bp sequence thus identified shows an interrupted homology (8 out of 15) with the wild-type core. The extent and arrangement of nonhomologous bases allow precise placement of the crossover point for this *recombination* to the +4 to +5 internucleotide bond of the core region. Sequences flanking the core region show no obvious homology with analogous sequences of the phage or primary bacterial *att* *sites*. Comparison of the galT left prophage *att* *site* with the analogous

wild-type site is of particular interest and is discussed in relation to binding studies with purified *int* protein.

**8/3,K/49 (Item 12 from file: 5)**
DIALOG(R)File 5:Biosis Previews(R)


0002665031 BIOSIS NO.: 197967054026
**STRUCTURE OF THE PHAGE LAMBDA-ATT SITES GENERATED BY *INT* DEPENDENT DELETIONS**
AUTHOR: HOESS R H (Reprint); LANDY A
AUTHOR ADDRESS: SECT MICROBIOL MOL BIOL, DIV BIOL MED, BROWN UNIV, PROVIDENCE, RI 02912, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 75 (11): p5437-5441 1978
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

**STRUCTURE OF THE PHAGE LAMBDA-ATT SITES GENERATED BY *INT* DEPENDENT DELETIONS**

ABSTRACT: Bacteriophage .lambda. integrates into the chromosome of its Escherichia coli host by a site-specific *recombination* between a locus on the phage chromosome (phage att site) and a locus on the bacterial chromosome (bacterial att site). The nucleotide sequence of 4 .lambda. att sites altered in site-specific *recombination* was determined. The *int*-dependent deletions that generated these *att* *sites* have 1 end point within the phage *att* *site* and extend either to the left or to the right. As a result of the new internucleotide bond created by deletion formation, these phage have...

...for regions to the left and .DELTA.' for regions to the right, do not share any discernible homology with their analogous counterparts in the phage *att* *site* arms, P and P', respectively, or with the bacterial *att* *site* arms, B and B', respectively. The finding of alterations in the 15 base-pair common core region necessitates a reinterpretation of the genetic properties of these att in site-specific *recombination*. The structure of these sites in relation to their genetic properties can be viewed as being consistent with a model in which the only specificity elements in *int*-dependent site-specific *recombination* are the common core region, O, and the phage arms, P and P'.

**8/3,K/50 (Item 1 from file: 73)**
DIALOG(R)File 73:EMBASE


10916706 EMBASE No: 2000415597
**Definition of the attI1 site of class 1 integrons**
Partridge S.R.; Recchia G.D.; Scaramuzzi C.; Collis C.M.; Stokes H.W.; Hall R.M.
R.M. Hall, CSIRO Molecular Science, Sydney Laboratory, PO Box 184, North Ryde, NSW 1670 Australia
AUTHOR EMAIL: ruth.hall@molsci.csiro.au
Microbiology ( MICROBIOLOGY ) (United Kingdom) 2000, 146/11 (2855-2864)
CODEN: MROBE ISSN: 1350-0872
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 36

Integron-encoded integrases recognize two distinct types of *recombination* site: *att*/ *sites*, found in integrons, and members of the 59-base element (59-be) family, found in the integron-associated gene cassettes. The class 1 integron *integrase*, IntI1, catalyses

*recombination* between attI1 and a 59-be, two 59-be, or two attI1 sites, but events involving two attI1 sites are less efficient than the reactions in which a 59-be participates. The full attI1 site is required for high-efficiency *recombination* with a 59-be site. It is 65 bp in length and includes a simple site, consisting of a pair of inversely oriented IntI1-binding...

...IntI1-binding sites designated strong and weak. However, a smaller region that contains only the simple site is sufficient to support a lower level of *recombination* with a complete attI1 partner and the features that determine the orientation of attI1 reside within this region. An unusual reaction between the attI1 site...
MEDICAL DESCRIPTORS:
genetic *recombination*; binding site; bacterial gene; gene cassette; enzyme activity; catalysis; Escherichia coli; gene fusion; nucleotide sequence; nonhuman; controlled study; article; priority journal

**8/3,K/51 (Item 2 from file: 73)**
DIALOG(R)File 73:EMBASE


02473015 EMBASE No: 1983067026
**Bacteriophage lambda *int* protein recognizes two classes of sequence in the phage *att* *site*: Characterization of arm-type sites**
Ross W.; Landy A.
Div. Biol. Med., Brown Univ., Providence, RI 02912 United States
Proceedings of the National Academy of Sciences of the United States of America ( PROC. NATL. ACAD. SCI. U. S. A. ) (United States) 1982, 79/24 I (7724-7728)
CODEN: PNASA
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH

**Bacteriophage lambda *int* protein recognizes two classes of sequence in the phage *att* *site*: Characterization of arm-type sites**
MEDICAL DESCRIPTORS:
*bacteriophage; *genetic *recombination*; *lysogenization

**8/3,K/52 (Item 3 from file: 73)**
DIALOG(R)File 73:EMBASE


01514739 EMBASE No: 1979236579
**Site-specific *recombination* in bacteriophage lambda: Structural features of recombining sites**
Landy A.; Hoess R.H.; Bidwell K.; Ross W.
Sect. Microbiol. Molec. Biol., Div. Biol. Med., Brown Univ., Providence, R.I. 02912 United States
Cold Spring Harbor Symposia on Quantitative Biology ( COLD SPRING HARBOR SYMP. QUANT. BIOL. ) (United States) 1979, 43/2 (1089-1097)
CODEN: CSHSA
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH

**Site-specific *recombination* in bacteriophage lambda: Structural features of recombining sites**

We have undertaken a study of the structures involved in *int*-dependent site-specific *recombination* and have previously reported the DNA sequences for each of the four primary *att* *sites*, POP', POB', BOP', and BOB'. Our results indicate that the phage *att* *site* and bacterial *att* *site* have in common a sequence 15 nucleotide pairs in length. The crossover event of integrative *recombination* must be within the limits (or at the boundaries) of this 'common-core' sequence, since it occurs unaltered in both the leftward and rightward prophage *att* *sites*. The

four sets of sequences, adjacent to the common-core region, are different from one another and hereafter will be referred to as 'arms' (P...

...understand the relationship of structure and function in the attachment sites, we have analyzed the structures of a number of different attachment sites: the altered *att* *sites* of four lambda delection phages, four secondary *att* *sites* located within the lambda chromosome, and one secondary *att* *site* in the E. coli galT gene. This paper provides and overview of the results of a number of experiments with these altered or secondary *att* *sites*.
MEDICAL DESCRIPTORS:
*bacteriophage; *genetic *recombination*; *virus *recombination*
?ds

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Set     Items   Description
S1        216   (ATT (W) SITE?) (S) (INTEGRASE OR INT)
S2         16   S1 AND (ATTB AND ATTP AND ATTR AND ATTL)
S3          6   RD (unique items)
S4          0   S1 AND (SEQUENCE (W) SPECIFIC (W) RECOMBINATION)
S5        144   S1 AND (RECOMBINATION)
S6         68   RD (unique items)
S7         57   S6 NOT PY>2000
S8         52   S7 NOT S3
?s s8 and review
              52  S8
         1625952  REVIEW
      S9       0  S8 AND REVIEW
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       23mar04 14:41:10 User259876 Session D602.2
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               $9.03  43 Type(s) in Format  3
            $9.03  43 Types
    $12.71  Estimated cost File155
            $4.14    0.739 DialUnits File5
              $21.00  12 Type(s) in Format  3
           $21.00  12 Types
    $25.14  Estimated cost File5
            $4.94    0.504 DialUnits File73
               $8.10  3 Type(s) in Format  3
            $8.10  3 Types
    $13.04  Estimated cost File73
            OneSearch, 3 files,  2.392 DialUnits FileOS
     $1.25  TELNET
    $52.14  Estimated cost this search
    $52.50  Estimated total session cost   2.481 DialUnits


### Status: Signed Off. (6 minutes)
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